

400	410	420	430	440	450	400	410	420	430	440	450
YGGSSHIWXSAXXHSHEQSSCRNKLÖNYDKR--	FTEGESHNY-----	RELLRECEYEI---				YGGSSHIWXSAXXHSHEQSSCRNKLÖNYDKR--	FTEGESHNY-----	RELLRECEYEI---			
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
460	470	480	490	500	510	460	470	480	490	500	510
-JNSPSXSPCKAPRSSLDRVCHAPQBSQAPAI	SCPBYHLVPALRYRCWDVPADLCNXYILV	HKMEFI-F-				-JNSPSXSPCKAPRSSLDRVCHAPQBSQAPAI	SCPBYHLVPALRYRCWDVPADLCNXYILV	HKMEFI-F-			
410	420	430	440	450	460	410	420	430	440	450	460
KAKGAVALSDFHMSSTDL-----	LNAKTVINDPLXKEMAMLSR----	IHHDPVKPRLRAVFWIEF				KAKGAVALSDFHMSSTDL-----	LNAKTVINDPLXKEMAMLSR----	IHHDPVKPRLRAVFWIEF			
470	480	490	500	510	520	470	480	490	500	510	520
LSKTXNNXKDKRGKIDLSKF-----	KDILMO--	XSCXFOPIRIWAKKQCYPHI	IYSVLLSXLSYLEFHDEHREVS	I		LSKTXNNXKDKRGKIDLSKF-----	KDILMO--	XSCXFOPIRIWAKKQCYPHI	IYSVLLSXLSYLEFHDEHREVS	I	
470	480	490	500	510	520	470	480	490	500	510	520
VMNHRKAKHLRYVAHDLTFQYHSLDVTG	FLACATVAFIITK-C	LCQVWKFEVYTGKKRD				VMNHRKAKHLRYVAHDLTFQYHSLDVTG	FLACATVAFIITK-C	LCQVWKFEVYTGKKRD			
600	610	620	630	640	650	600	610	620	630	640	650
SHSFVAFSXVCLLSLTILXHKDMNTSKFSY	FYHCHHDVITSLTSDRVCNMLIPGVC	ITWMAKRSKCKI				SHSFVAFSXVCLLSLTILXHKDMNTSKFSY	FYHCHHDVITSLTSDRVCNMLIPGVC	ITWMAKRSKCKI			
670	680	690	700	710	720	670	680	690	700	710	720
HKIQXTQIÖNEAFYDLSLXVTKXFFFLNK	MFYIPISITDLRÖXIAKNDRBALHSEKAF	IPIHTRSSCHSL				HKIQXTQIÖNEAFYDLSLXVTKXFFFLNK	MFYIPISITDLRÖXIAKNDRBALHSEKAF	IPIHTRSSCHSL			
740	750	760	770	780	790	740	750	760	770	780	790
HFCCHLTDIFCVFLMTINROFLLSSNNK	RXNFXLTXRCPKPDIOVKÖILLRKYTT	IRNKKXLXLLXNPNXXYX				HFCCHLTDIFCVFLMTINROFLLSSNNK	RXNFXLTXRCPKPDIOVKÖILLRKYTT	IRNKKXLXLLXNPNXXYX			
810	820	830	840	850	860	810	820	830	840	850	860
TXPRCLFPMKMMNHNYSYLXÖKYNLLX	KNKEMVLVKKKKKKKTLSCRYAVARXOP	TVAPLRISISLTATLSC				TXPRCLFPMKMMNHNYSYLXÖKYNLLX	KNKEMVLVKKKKKKKTLSCRYAVARXOP	TVAPLRISISLTATLSC			
890	900	910				890	900	910			
RYVAYRXÖCHALRYRXÖCHAVYKRIYDS	KTLSLXAVTX					RYVAYRXÖCHALRYRXÖCHAVYKRIYDS	KTLSLXAVTX				

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-075614.res made by jdelaval on Sun 2 Sep 10 10:53:21 PDT.

query sequence being compared: US-09-784-340-1 (1-2759)

Number of sequences searched:
Number of scores above cutoff:

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : 075614.pep

100	-	
N	-	
U	-	
50	-	
M	-	
B	-	
E	-	
R	-	
O	-	
10	-	
F	-	
S	-	
E	-	
O	-	
5	-	
U	-	
E	-	
N	-	
C	-	
E	-	
S	-	
0	-	
SCORE	0	
STDEV	31	
	61	
	92	
	123	
	153	
	184	
	215	
	245	
	276	
		*

PARAMETERS

	Unitary	K-tuple
Similarity matrix	6	20
Translation Frame	1	Joining penalty
Mismatch penalty	1.00	Window size
Gap penalty	0.05	32
Gap size penalty		
Cutoff score	1	
Randomization group	0	

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	276	0	0.00

Times:	CPU	Total Elapsed
	00:00:00.00	00:00:00.00

```

Number of residues:      528
Number of sequences searched: 1
Number of scores above cutoff: 1

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The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

> O <
01 10 Intelligenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-075614.res made by jdelaval on Sun 2 Sep 101 10:53:28-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File: 075614.pep

100-
N -
U -50-
M -
B -
E -
R -
O -
F 10-
S -
E 5-
Q -
U -
E -
C -
N -
S -
E -
S 0-
SCORE 0 1 2 3 4 5 6 7 8 9
STDEV

PARAMETERS
Similarity matrix Unitary K-tuple 2
Translation Frame 6 Joining penalty 20
Mismatch penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS
Scores: Mean Median Standard Deviation
9 0 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 528
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. 075614	UDP GLUCURONOSYLTRANSFERASE 2	528	9	68	0.00	3

1. US-09-784-340-1 (1-2759)
075614 UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.

TOIG of: 075614 check: 5913 from: 1 to: 528
ID 075614 PRELIMINARY; PRT; 528 AA.
AC 075614
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.
GN UGT2B4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93326164; PubMed=8333863;
RA Jin C.J., Miners J.O., Lillywhite K.J., Mackenzie P.I.;
RT "CDNA cloning and expression of two new members of the human liver
RT UDP-glucuronosyltransferase 2B subfamily."
RL Blochem. Biophys. Res. Commun. 194:496-503(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mackenzie P.I.;
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF081793; AAC32272.1;
DR InterPro; IPR002213;
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase.
SQ SEQUENCE 528 AA; 60497 MW; B6F5BA0705E952C4 CRC64;

075614 Length: 528 September 2, 2001 10:50 Type: P Check: 5913 ..

Initial Score = 9 Optimized Score = 68 Significance = 0.00
Residue Identity = 17% Matches = 92 Mismatches = 327
Gaps = 112 Conservative Substitutions = 0
Translation Frame = 3 X 10 20

MSMKWTSAALLIQLSCYFSSGCGKVLVWPTFESHWNKIKTILDELVORCHEVYLAASSASISFDPNSPSTL
10 20 30 40 50 60 70 80
30 40 50 60 70 80
SSVLAVDSYVK-----SNGCPYTXAIGIMSRSP--XKSSXHEM-----RQXYLIQS---LRXLTIGSL
80 90 100 110 120 130 140
KEEVYVPSLKTTEFEDIKQLVKRMALPKDIFWSTLSQVQELMTFNDILRFCKDIVSNKKLKKLQDESR
90 100 110 120 130 140
LHXNLRWSTICRTEQKKMYLLTXLMSCQAY-----QPGNQLXNMKIFILKKKELKKXCVKRLS-----TIR
150 160 170 180 190 200 210
FDVVLADAVPFGE-----LLAEILKIPFVYSLNRPSTGALFKHSGGLFPFPPSYPVVMSLSDMQTIER
150 160 170 180 190 200 210
150 160 170 180 190 200 210
VKNMIVLVYEEFWFOIFDKKKWQDFSEVIGRPTTLSETMAKADWLIRNYWDFQ--FRAPLPNVPEFVGL
220 230 240 250 260 270 280

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. 075614	UDP GLUCURONOSYLTRANSFERASE 2	528	5	81 0.00 4

1. US-09-784-340-1 (1-2759)
075614 UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.

TOIG of: 075614 check: 5913 from: 1 to: 528

ID 075614 PRELIMINARY: PRT: 528 AA.

AC 075614;
DC 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.
CN UGT2B4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE=93326164; PubMed=8333863;
RX Jin C.J., Miners J.O., Lillywhite K.J., Mackenzie P.I.;
RT "cDNA cloning and expression of two new members of the human liver
"UDP-glucuronosyltransferase 2B subfamily."
RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
RN 12
RP SEQUENCE FROM N.A.
RA Mackenzie P.I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081793; AAC3272.1;
DR InterPro: IPR002213;
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferase.
SQ SEQUENCE 528 AA: 60497 MW; B6F5BA0705E952C4 CRC64;

075614 Length: 528 September 2, 2001 10:50 Type: P Check: 5913

Initial Score = 5 Optimized score = 81 Significance = 0.00
Residue Identity = 17% Matches = 107 Mismatches = 365
Gaps = 131 Conservative Substitutions = 0
Translation Frame= 4

```

RYVTADSVLSTIRVYTAQCCQRYARNAXCCQRYATXRHDSVAVNDMLRMGMTVGCQRYATXRHDSVFF
80 90 100 110 120 130
FFFTPTSTSLFFPYSLKLYKXKXELXVFTILKNRLNVOYQAKFY-----KIRNRYNHIEFLMTYLIKII
MSMKWTSL-----LLIQ-----LSCYSSGSGCKVLWPTFESHMMNKTI
X 10 20 30 40
140 150 160 170 180 190 200
CLTXISYGFHLYRKPQPLLPEDNNKCLFIFKNTQKMSYKWKMCRLXHLDEVCGNIANYSECNALSSFL
110 120 130 140 150 160 170
FMSYLSVOVEIMTFTNDILKKFKCKDIYSNKKLKKLOESFDDVVLADAVFPFSELLAEILKI-PRYYSLSRFS
180 190 200 210
LDELVORGHEVTVLASSASISFDPN-----SPSTLKEEVYFVSLTKTEFEDITKQLYKRNAAE--LPKDT
50 60 70 80 90 100
210 220 230 240 250 260 270
AIIHCLASVMIGMKGKLEKL-KKKNHVYTNHKLK-SXNASLICV---YXILKILHLLIYIHVF---QT
110 120 130 140 150 160 170
PGISIILOVTLST-----KVRVETMSWKQXQKXKXNDLVFMSLCHKVREESKHTXENATREKXIDILITSXSWNS
180 190 200 210 220 230 240 250 260 270

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PGYAIKHSGLLEPPSYVPPVM-----SELSD-QMTFIERV---KNMIYVLYEEFEPQIPDMKMD
180 190 200 210 220 230
340 350 360 370 380 390 400 410
RLVYSXDKITEXIILKKXGFEHQIILCGMNXODYPIRSPFLNLSRSPISFSEFYXIIIPDKIKIILXTRIXOLPH
110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300
QFSEVIGRPPTLSETMAKADIWLIRRYWDFOPFPHPLPNEVFVGSLCKPAKPLPKRMK-----EFVYSSG
420 430 440 450
RSACTOSHLS-SAGTRXGHSGLIAGAWILCGANQOTRSR-----LIDL-----GALQVD-----
310 320 330 340 350 360 370
ENGYYVPSLSGMSVNTSEERANVLASA--LAKIPQKVLNMRDGNKPDPTLGINRLRYKIQNDLHGPKPRA
460 470 480 490 500 510 520
---HGEPLIT---SXHSIKYRNRKXALFSKPSVNLRLSXPSLFIQLLWPSCELCYQADHQIWLPLPXGPHG
380 390 400 410 420 430 440
FITHGANGIYEATYHGIPIWGVPLADQDPNIAHMKAKGANA5LDFHTWSSITDLNALKTIVINDPLIKENA
530 540 550 560 570 580 590
KXILRSFSFHHEXXK-----LMFW-DQEDHSGVSNHTAEEYWLMMWVFEICTSITPSVSGGGLKQXXPFL
450 460 470 480 490
MKLSRIH--HDQPVKPLDRAVFEWIEFVNRHKGAKHLRYAHDLTW---FOYHS-----LDVTGFL
600 610 620 630 640 650 660
LXHEFYEPKTPQYHILPLNSGQNPFPXAKLMQVYSAIIQQTOSXGMYEIONPMFVLAIISQLFPQSHI
500 510 520 530
LACVATVLEIIT---KCLFCVWKFEVRTGKKGRD
670 680 690 700 710 720 730
MXMAFLMPTTYKTLPRNDSRNPESRSGTKALNLFLEPERSFCILVLSAQVHHKVELEVSHSFAPCLLQK
740 750 760 770 780 790 800
FXVXQKGLQATQPSGLHRESQGLALHRSWFPVASSASDCRKSSTHSFLAKFLFQOKNHLIILXILARLIS
810 820 830 840 850 860 870 880
LARHSELQQIFHFLFPCPVAVGPPQISMOKASCQSLTKALSESILPBHGSLXALLLEXPYHXANGSCHRAY
890 900 910
PGLSHRIHSOHRRAAGAEIPKULTCOTSTXWQFPHILCN

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CKPAKPIPKKKKEVSSGNGVVFVSL-----GSMVSNNT-----SEERANV-----IASALAKIPQVLMR
290      300      310      320      330      340
-----SVMPYRHFHXOFIVXDQXCMVCRRA-YLNKKRKILIMLITSCXRMMLHXFWFTEFCEFYI---F
210      220      230      240      250      260
FDGKMPDLGLNTRILYKMKIPQNDLGHKTRAFITHGANGIYEAI---YHGIPVGVPLADOPDNIAHMK
340      350      360      370      380      390      400
270      280      290      300      310      320
YFETSMCKHQESAYCSPPYHL-----RLEKXXRHGNSDIRNKRKIMVSCPCVTKKKEKRVSTPRKM
AKGAVALSDPFTMS-----STDLLNLKTVINDPLKENAMKLSRIHHQOPKPLDRAFWIE---FVNRHKG
410      420      430      440      450      460      470
330      340      350      360      370      380      390
RKNEIYSOPHDHGIIGYIAKIKXONRXENSKVPTKF---YVAGINRITPQSLSXIMWDLPEFLYSFIKF
480      490      500      510      520      530
AK-HLRVAHDLTWFOY-----HSLDVTGFLACAVATIFI-----ITKCLF-----CVMKF
400      410      420      430      440      450      460
-LTGKXKTFCEOEYSSCHTGOEPNHIYRVLEPGEVNGSXQVLGSFVAHDKLDPEDCSIXGLYRLIMVNS
520      530
VRTGKKKKRD
X
470      480      490      500      510      520      530
XXSHSILFIRIGINDCSOSPOXIFACHSEFVYFSCSGLHVSYYIKLITKYGNSHHNDPMVNSFIDPIHST
540      550      560      570      580      590      600
MSDKSFEGFMKRIILGPIIPIQPSIGSCMGWFSFVPPXHLMLDGGKXNDISLFCNLIKQXPOKHHNT
610      620      630      640      650      660      670
IFPXTLDKIFHFLROSFRFTYQSSNKLKVLWLKFKRIPICSYXPIYLSFSHSLTXCSGSPSXCILTKLPK
680      690      700      710      720      730      740      750
MIVVLINPEVEQNKKHXLFFSYQKSHVSCXCHRRRYIGKMSKFPPTASLHASYRNSKCEHKRDCKOLSHQ
760      770      780      790      800      810      820
VSTGNHRYKHIYVGFLLXLLKRLIVDKALTHHFXSSSYFNKKIIXFYNKXLPGXAXAMODIOSXVKNKTIFF
830      840      850      860      870      880      890
CSVLHMDHLKFQCRRLPVNXXRRLXVSQCYLMAHSYELFXNDIDIKPMAHVTPGHODPTESTANTELO
900
EOKYOS

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-075614.res made by jdelaval on Sun 2 Sep 101 10:53:50-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : 075614.pep

```

100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
S -
E 5-
O -
U -
E -
N -
C -
E -
S 0-
SCORE 0 1 2 2 3 4 5 5 6 7
STDEV

```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Translation frame	6		
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	7	0	0.00
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00
Number of residues:		528	
Number of sequences searched:		1	
Number of scores above cutoff:		1	

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Sig. Frame
1. 075614	UDP GLUCURONOSYLTRANSFERASE 2	528	7	75 0.00 6

1. US-09-784-340-1 (1-2759)
075614 UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.

TOIG of: 075614 check: 5913 from: 1 to: 528

ID 075614 PRELIMINARY; PRT; 528 AA.
AC 075614;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.
GN UGT2B4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93326164; PubMed=8333863;
RA Jin C.J., Miners J.O., Lillywhite K.J., Mackenzie P.I.;
RT "cDNA cloning and expression of two new members of the human liver
UDP-glucuronosyltransferase 2B subfamily";
RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mackenzie P.I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF081793; AAC32272.1;
DR InterPro; IPR002213;
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase.
SQ SEQUENCE 528 AA: 60497 MW: B6F5BA0705E952C4 CRC64;

075614 Length: 528 September 2, 2001 10:50 Type: P Check: 5913 ..
Initial Score = 7 Optimized Score = 75 Significance = 0.00
Residue Identity = 18 Matches = 101 Mismatches = 339
Gaps = 98 Conservative Substitutions = 0
Translation Frame= 6

		X	10	20	
MSKMTSALLLIQISCTFFSSGSGCKVLVPTFERSHMKNTITLDELVOGHEVTVLASSSISFDPNPSTL	10	20	30	40	50
30	40	50	60	70	80
RSXMTV-LSTIRVYTAQCRCQRYATYRHD---SGLS---TIRYVTAQCFFPFYFQKNHLFILOXII					
KFEYPPYSLKTEFEDIKQVYKRMALPKDFTWSYLSQVQELMTFNDILRKCAIVSKKLMKLO---	80	90	100	110	120
90	100	110	120	130	140
LLIETIRMSIHHEKREYFKSVLSIKLKNOKLOS-HISNGY---LSQNNLPLNLTMTFSLCKKISVSF					
-----ESR--FDVYIADAVFPFGELLAALLKIPFYSLRFSGYAIEKHSGGLFPFPPSYVPMVMSLSDQMTF	150	160	170	180	190
160	170	180	190	200	210
I-----IXGXQXELSLIYHOEHFK---NVSXVMAEMXAMTSRKGMKYSKLFYXCPVIFSNLSLSEISNAG					
IERYKNNIYLYFEFNFQIDMKWDQFYSEV---IGRPTLSEFMAKADIMLIRNYWDQFPFPHL--LPNVE	210	220	230	240	250
210	220	230	240	250	260
					270

220	230	240	250	260	270	280
YVESGLIXIEKEKSLCYSQANVIECFIDLCGLNFVNFPTFSLHPCV-----CANTRNOHIAHGPIITGX						
FGGL-HCKRAKPL-----PKKKKEFQSSGNGVYF-----SIGSVNSTSEERANVASALAKIPQKYLW	280	290	300	310	320	330
290	300	310	320	330	340	350
RSNDVMEYVISEIGKFRICIHVLVSQSERREXAHGKCNEMRYTHNLIMEFYAIXLRXNNRINMKIARFS						
R-----FDGNKRDITGINTRLKWIPIQ-----NDLLGHKPTRAFITHGANCIYEAI-YHGIPMGVPLLDAP	340	350	360	370	380	390
360	370	380	390	400	410	420
PNSMWLELTGLPHQVLEFGKITYSLFSIFLVLLNFXQENKHKHFVNKNIAVATQVSR-----NPITSIEXC						
DNLAHMAKQ--AAVSLDFITMS-----IDLNALKTIVINDPLYK--ENAMKLSRIHHQPKPIIDRAVFW	410	420	430	440	450	460
430	440	450	460	470	480	490
MNOY-RSMADRRCLA---PLMNTNSIQKTARSRGFTGXSWILDLNLIASF--XESVYTVLKALSKSSL						
IEFYMRKKGAKHLRVAHADLTWFOYHSLDYF---GFLACVATVIFITIKCLFCYWKFPRTGKKGRD	470	480	490	500	510	520
490	500	510	520	530	540	550
VIVLKEFISTAPLAFMXAMLSXSPNMGFTTIGPMXIASXIPFIPXVIALVLGXPRRSFGIQSRYVL						
570	580	590	600	610	620	630
APNVDFEFLYLNHTFCGIWARAEAMILAFSVTFKNSDPRENTTIPSSPELMTKFSISLGKALAGLCNPP						
640	650	660	670	680	690	700
TNSKLGWYXGNSKSGQYVRISHISAFPTVSHNVGLPMNLLXNSQKXSXIXOKMKNKTESIEFPTLSKV						
710	720	730	740	750	760	770
ILSVSPVIGTGYESGAGSPFQRLRSIIPTEILISVSTKGTASNAIRSPQGTGSGISITSXLVSCSFPISVX						
780	790	800	810	820	830	840
LXIKLSHIFKVPILSTKSKSFNFTTDCQVDKPKTFARASTNISFSSVLSGIMWTSNFMNAEGFLXSINEGF						
850	860	870	880	890	900	910
EXVNTVTSMPLTMSSSHMTLTLSQWLMSSGHTPTFPONPOPTOKSCSRNTKADLSDLMAAVSHDLOW						

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